

Figure 1 (A-F)

Construct Forms Comprising at Least one Single-Stranded Region

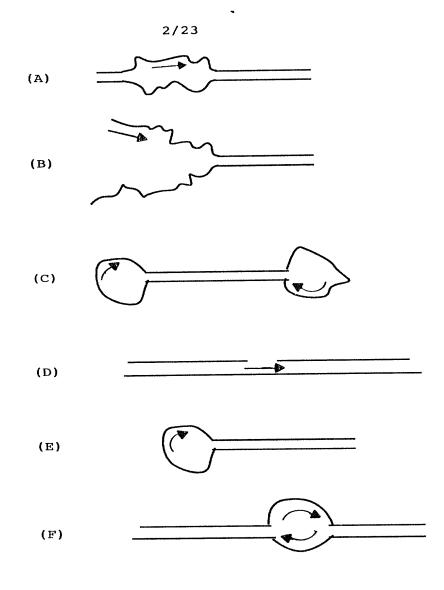


Figure 2 (A-F)

Functional Forms of the Construct

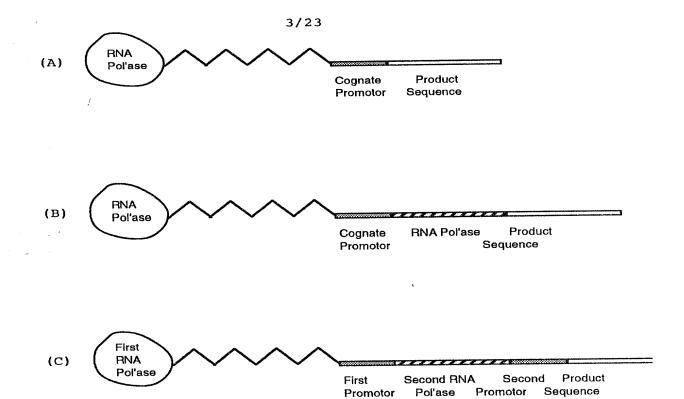


Figure 3 (A-C)

Three Constructs with an RNA Polymerase Covalently Attached to a Transcribing Cassette

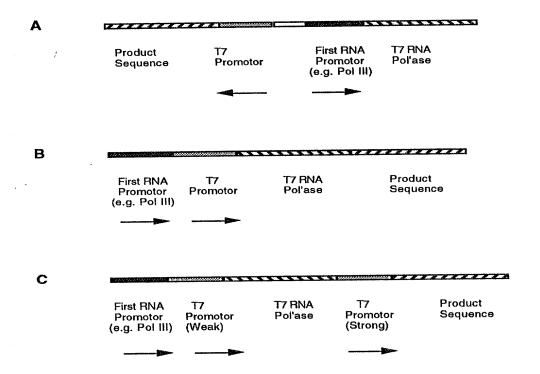


Figure 4 (A-C)

Three Constructs with Promoters for Endogenous RNA Polymerase

M13mp18. Seq Length: 7250 1. **AATGCTACTA** CTATTAGTAG **AATTGATGCC** ACCTTTTCAG CTCGCGCCCC **AAATGAAAAT ATAGCTAAAC AGGTTATTGA** CCATTTGCGA 51. **AATGTATCTA ATGGTCAAAC** TAAATCTACT **CGTTCGCAGA ATTGGGAATC AACTGTTACA** 101. **TGGAATGAAA** CTTCCAGACA **COGTACTITA GTTGCATATT** TAAAACATGT 151. CACCAGATTC **AGCAATTAAG** CTCTAAGCCA TOOGCAAAAA 201 TGAGCTACAG 251 TGACCTCTTA TCAAAAGGAG CAATTAAAGG **TACTCTCTAA** TOCTGACCTG 301. TTGGAGTTTG CITCOGGICT GGTTCGCTTT GAAGCTCGAA TTAAAACGCG 351. **ATATTTGAAG** TCTTTCGGGC TTCCTCTTAA **TCTTTTTGAT GCAATCCGCT** TTGCTTCTGA **CTATAATAGT** CAGGGTAAAG **ACCTGATTTT TGATTTATGG** 401. **TCATTCTCGT** TTTCTGAACT **GTTTAAAGCA** TTTGAGGGGG **ATTCAATGAA** 451. **TATTGGACGC TATCCAGTCT** 501. **TATTTATGAC** GATTCCGCAG **AAACATTTTA** 551. CTATTACCCC CTCTGGCAAA **ACTICITITIE** CAAAAGCCTC TCGCTATTTT **GGTTTTTATC GICGICIGGT AAACGAGGGT TATGATAGTG** TTGCTCTTAC 601. 651. TATGCCTCGT **AATTCCTTTT GGCGTTATGT ATCTGCATTA GTTGAATGTG GTATTCCTAA ATCTCAACTG ATGAATCTTT CTACCTGTAA TAATGTTGTT** 701. 751. COGTTAGTTC **GTTTTATTAA CGTAGATTTT** TCTTCCCAAC **GTOCTGACTG GTATAATGAG CCAGTTCTTA AAATCGCATA AGGTAATTCA** 801. CAATGATTAA 851. **AGTTGAAATT AAACCATCTC AAGCCCAATT TACTACTOGT** TCTGGTGTTC TOGTCAGGGC **AAGCTTATT** 901. CACTGAATGA **GCAGCTTTGT** TACGTTGATT 951. **TGGGTAATGA ATATCCGGTT CTTGTOGAAG ATTACTCTTG ATGAAGGTCA** 1001 GCCAGCCTAT GOGOCTGGTC **TGTACACCGT TCATCTGTCC TCTTTCAAAG** 1051 TTGGTCAGTT **CGGTTCCCTT ATGATTGACC** GICIGOGOCT COTTOCCOCT 1101 AAGTAACATG GAGCAGGTOG **CGGATTTCGA** CACAATTTAT CAGGOGATGA 1151 TACAAATCTC CGTTGTACCTT TGTTTCGCGC **TTGGTATAAT** COCTOCOCC 1201 CAAAGATGAG **TGTTTTAGTG** TATTCTTTCG **CCTCTTTCGT** TTTAGGTTGG

Figure 5

1251	TGCCTTCGTA	GTGGCATTAC	GTATTTTACC	CGTTTAATCG	AAACTTCCTC
1301	ATGAAAAAGT	CTTTAGTCCT	CAMAGCCTCT	GTAGCCGTTG	CTACCCTCGT
1351	TOOGATGCTG	TCTTTCGCTG	CTGAGGGTGA	OGATOCCOCA	AAAGOGGOCT
1401	TTAACTCCCT	GCAAGCCTCA	GOGACOGAAT	ATATOGGTTA	TOOGTGGGGG
1451	ATGGTTGTTG	TCATTGTOGG	CGCAACTATC	GGTATCAAGC	TGTTTAAGAA
1501	ATTCACCTCG	AAAGCAAGCT	GATAAACCGA	TACAATTAAA	GECTCCTTTT
1551	GGAGCCTTTT	TTTTTGGAGA	TTTTCAACGT	GAAAAAATTA	TTATTCGCAA
1601	TTCCTTTAGT	TGTTCCTTTC	TATTCTCACT	COCCTGAAAC	TGTTGAAAGT
1651	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA	TTTACTAACG	TCTGGAAAGA
1701	CGACAAAACT	TTAGATCGTT	ACCCTAACTA	TGAGGGTTGT	CTGTGGAATG
1751	CTACAGGCGT	TGTAGTTTGT	ACTGGTGACG	AAACTCAGTG	TTACGGTACA
1801	TOGGTTOCTA	TTGGGCTTGC	TATCCCTGAA	AATGAGGGTG	GTGGCTCTGA
1851	GGGTGGCGGT	TOTGAGGGTG	GOGGTTCTGA	cecirecceci	ACTAAACCTC
1901	CTGAGTACGG	TGATACACCT	ATTOCGGGCT	ATACTTATAT	CAACCCTCTC
1951	GACGGCACTT	ATCOGCCTGG	TACTGAGCAA	AACCCGCTA	ATCCTAATCC
2001	TTCTCTTGAG	GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	CAGAATAATA
2051	GGTTCCCGAAA	TAGGCAGGGG	GCATTAACTG	TTTATACGGC	CACTGTTACT
2101	CAAGGCACTG	ACCCCGTTAA	AACTTATTAC	CAGTACACTC	CTGTATCATC
2151	AAAAGCCATG	TATGACGCTT	ACTOGAACOGG	TAAATTCAGA	GACTGCGCTT
2201	CAAGGCACTG	ACCCCGTTAA	AACTTATTAC	CAGTACACTC	CTGTATCATC
2151	AAAAGCCATG	TGCCTCAACC	TCCTGTCAAT	OCTOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	eciciegieg
2201	TCCATTCTGG	CTTTAATCAA	GATOCATTOG	TTTGTGAATA	TCAAGGCCAA
2251	TOGTCTGACC	TGCCTCAACC	TCCTGTCAAT	ecteecesce	ecticitedies
2301	TEGITCIEGT	eeceectictic	AGGGTGGTGG	CTCTGAGGGT	eccentricie
2351	AGEGTGGCGG	CTCTGAGGGA	CCCCCCTTCCCC	GIGGIGGCIC	TEGTTCCGGT
2401	GATTTTGATT	ATGAAAAGAT	GGCAAACGCT	AATAAGGGGG	CTATGACOGA
2451	AAATGCCGAT	GAAAAACGCCGC	TACAGTCTGA	COCTAMAGEC	AAACTTGATT

Figure 5

2501 C	IGTOGCTAC	TGATTACGGT	GCTGCTATOG	ATGGTTTCAT	TOGTGACGIT
2551 TO	DOGGOCTTG	CTAATGGTAA	TEGTECTACT	GGTGATTTTG	CTGGCTCTAA
2601 T	TOOCAAATG	GCTCAAGTCG	GTGACGGTGA	TAATTCACCT	TTAATGAATA
2651 A	TTTCCGTCA	ATATTTACCT	TOCCTOCCTC	AATOGGTTGA	ATGTOGOCCT
2701 T	TTGTCTTTA	GOGCTGGTAA	ACCATATGAA	TTTTCTATTG	ATTGTGACAA
2751 A	ATAAACTTA	TICCGIGGIG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT
2801 T	TATGTATGT	ATTTTCTACG	TTTGCTAACA	TACTGCGTAA	TAAGGAGTCT
2851 T	TATCATGCC	AGTTCTTTTG	GGTATTCCGT	TATTATTGCG	TTTCCTCGGT
2901 T	тесттетев	TAACTTTGTT	OGGCTATCTG	CTTACTTTTC	TTAAAAAGGG
2951 C	ттосатала	ATAGCTATTG	CTATTTCATT	GTTTCTTGCT	CTTATTATTG
3001	ECTTAACTC	AATTCTTGTG	GGTTATCTCT	CTGATATTAG	CGCTCAATTA
3051	COCTCTGACT	TIGTTCAGGG	TGTTCAGTTA	ATTCTCCCGT	CTAATGCGCT
3101 7	CCCTGTTTT	TATGTTATTC	TCTCTGTAAA	GECTECTATT	TTCATTTTTG
3151 /	ACGTTAAACA	AAAAATCGTT	TCTTATTTGG	ATTGGGATAA	ATAATATGGC
3201	TGTTTATTTT	GTAACTGGCA	AATTAGGCTC	TOGAMAGACG	CTOGTTAGOG
3251	TTGGTAAGAT	TCAGGATAAA	ATTGTAGCTG	GGTGCAAAAT	AGCAACTAAT
3301	CTTGATTTAA	GGCTTCAAAA	OCTOCOGCAA	GTCGGGAGGT	TOGOTAAAAC
3351	ecctoeccit	CTTAGAATAC	COGGATAAGCC	TTCTATATCT	GATTTGCTTG
3401	CTATTGGGGG	CGGTAATGAT	TOCTACGAATO	AAAAATAAAA G	COCCTTCCTT
3451	GTTCTCGATG	AGTGCGGTAC	TTGGTTTAAT	ACCOGTTCTT	GGAATGATAA
3501	GGAAAGACAG	COGATTATTG	ATTGGTTTCT	ACTOCTOGT	AAATTAGGAT
3551	GGGATATTAT	тттсттвтт	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG
3601	COTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TGGACAGAAT
3651	TACTTTACCT	TTTGTCGGTA	CTTTATATTC	TCTTATTACT	GOCTOGAAAA
3701	тесстстесс	TAAATTACAT	г аптесоатта	TTAAATATGG	CGATTCTCAA
3751	TTAAGCCCTA	CTGTTGAGCC	TTGGCTTTAT	ACTGGTAAG/	ATTTGTATAA
3801	OGCATATGAT	ACTAMACAGO	CTTTTCTAG	TAATTATGAT	TCCGGTGTTT

Figure 5

3851	ATTCTTATTT	AACGCCTTAT	TTATCACACG	GTCGGTATTT	CAAACCATTA
3901	AATTTAGGTC	AGAAGATGAA	ATTAACTAAA	ATAATATTGA	AAAAGTTTTC
3951	TOGOGITICIT	TGTCTTGCGA	TTGGATTTGC	ATCAGCATTT	ACATATAGTT
4001	ATATAACCCA	ACCTAAGCCCG	GAGGTTAAAA	AGGTAGTCTC	TCAGACCTAT
4051	GATTTTGATA	AATTCACTAT	TGACTCTTCT	CAGCGTCTTA	ATCTAAGCTA
4101	TOGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	AGCGACGATT
4151	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC
4201	ATTAAAAAAG	GTAATTCAAA	TGAAATTGTT	AAATGTAATT	AATTTTGTTT
4251	TCTTGATGTT	TGTTTCATCA	тсттсттта	CTCAGGTAAT	TGAAATGAAT
4301	AATTOGOCTC	TGCGCGATTT	TGTAACTTGG	TATTCAAAGC	AATCAGGCGA
4351	AATCCGTTATT	GTTCTCCCCG	ATGTAAAAGG	TACTGTTACT	GTATATTCAT
4401	CTGACGTTAA	ACCTGAAAAT	CTACGCAATT	TCTTTATTTC	TGTTTTACGT
4451	GCTAATAATT	TTGATAATGGT	TGGTTCAATT	CCTTCCATAA	TTCAGAAGTA
4501	TAATCCAAAC	AATCAGGATT	ATATTGATGA	ATTGCCATCA	TCTGATAATC
4551	AGGAATATGA	TGATAATTCC	ectecttete	GIGGITTCTT	TGTTCCGCAA
4601	AATGATAATG	TTACTCAAAC	TTTTAAAATT	AATAACGTTC	GGGCAAAGGA
4651	TTTAATACGA	GTTGTCGAAT	TGTTTGTAAA	GTCTAATACT	TCTAAATCCT
4701	CAAATGTATT	ATCTATTGAC	GGCTCTAATC	TATTAGTTGT	TAGTGCTCCT
4751	AAAGATATTT	TAGATAACCT	TOCTCAATTC	CTTTCTACTG	TTGATTTGCC
4801	AACTGACCAG	ATATTGATTG	AGGGTTTGAT	ATTTGAGGTT	CAGCAAGGTG
4851	ATGCTTTAGA	TTTTCATTT	actigation	CTCAGOGTGG	CACTGTTGCA
4901	GCCGCTGTTA	ATACTGACCG	OCTCAOCTCT	GTTTTATCTT	CTECTEGTEG
4951	TTCGTTCGGT	ATTTTTAATG	GOGATGTTTT	AGGGCTATCA	GTTOGOGCAT
5001	TAAAGACTAA	TAGOCATTCA	AAAATATTGT	CTGTGCCACG	TATTCTTACG
5051	CTTTCAGGTC	AGAAGGGTTC	TATCTCTGTT	GGCCAGAATG	TOCCTTTTAT
5101	TAAAGACTAA	TAGCCATTCA	AAAATATTGT	CTGTGCCACG	TATTCTTACG
5151	CGATTGAGCG	TCAAAATGTA	GGTATTTCCA	TGAGCGTTTT	TOCTGTTGCA

Figure 5

5201	ATGGCTGGCG -	GTAATATTGT	TCTGGATATT	ACCAGCAAGG	CCGATAGTTT
5251	GAGTTCTCT	ACTCAGGCAA	GTGATGTTAT	TACTAATCAA	AGAAGTATTG
5301	CTACAACGGT	TAATTTGCGT	GATGGACAGA	CTCTTTTACT	COGTICACCTC
5351	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GGOGTACOGT	TOCTGTCTAA
5401	AATOCCTTTA	ATCGGCCTCC	TGTTTAGCTC	COGCTCTGAT	TOCAAOGAGG
5451	AAAGCACGTT	ATACGTGCTC	GTCAAAGCAA	CCATAGTACG	OGCOCTIGITAG
5501	CGGCGCATTA	ACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GIGIGGIGGI	TACGCGCAGC	GTGACCGCTA
5551	CACTTGCCAG	COCCTAGOG	CCCCCTCCTT	TCGCTTTCTT	CCCTTCCTTT
5601	CTCGCCACGT	TOGOCGGCTT	TCCCCCGTCAA	GCTCTAAATC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
5651	TTTAGGGTTC	CGATTTAGTG	CTTTACGGCA	OCTOGACCCC	AAAAAACTTG
5701	ATTTGGGTGA	TEGTTCACGT	AGTGGGCCAT	CCCCTGATA	GACGGTTTTT
5751	CGCCCTTTGA	COTTIGGAGTC	CACGTTCTTT	AATAGTGGAC	TCTTGTTCCA
5801	AACTGGAACA	ACACTCAACC	CTATCTCGGG	CTATTCTTTT	GATTTATAAG
5851	GGATTTTGCC	GATTTCGGAA	CCACCATCAA	ACAGGATTTT	COCCTECTEG
5901	GGCAAACCAG	OGTGGACOGC	TTGCTGCAAC	TCTCTCAGGG	OCAGGOGGTG
5951	AAGGGCAATC	AGCTGTTGCC	OGICTOGCTG	GTGAAAAGAA	AAAOCACOCT
6001	GGCGCCCAAT	ACGCAAACCG	CCTCTCCCCCG	COCCTTOCCC	GATTCATTAA
6051	TECAGCTEGC	ACGACAGGTT	TOOOGACTEG	AAAGOGGGCA	GTGAGCGCAA
6101	CGCAATTAAT	GTGAGTTAGC	TCACTCATTA	GGCACCCCAG	GCTTTACACT
6151	TTATGCTTCC	GECTICGTATG	TIGIGIGGAA	TIGIGAGOGG	ATAACAATTT
6201	CACACAGGAA	ACAGCTATGA	CCATGATTAC	GAATTOGAGC	TOGGTACCCG
6251	GOGATOCTCT	AGAGTOGACO	TECAGECATE	CAAGCTTGGC	ACTIGGOOGTIC
6301	GTTTTACAAC	GTOGTGACTG	GGAAAACCCT	GGOGTTACCC	AACTTAATOG
6351	OCTTGCAGCA	CAATCCCCTT	TOGOCAGCTG	GOGTAATAGC	GAAGAGGCCC
6401	GCACCGATCG	COCTTCCCAA	CAGTTGCGCA	GOCTGAATGG	CGAATGGCGC
6451	TTTGCCTGGT	TTCCGGCACC	AGAAGCGGTG	COGGAMAGCT	COCTOCACTO
6501	CGATCTTCCT	GAGGCCGATA	œgrægrægr	CCCCTCAAAC	TERCAGATEC

Figure 5

6551	ACGGTTACGA	TGCGCCCATC	TACACCAACG	TAACCTATCC	CATTACGGTC
6601	AATOOGOOGT	TTGTTCCCAC	GGAGAATOOG	ACGCGTTGTT	ACTOGCTCAC
6651	ATTTAATGTT	GATGAAAGCT	GECTACAGGA	AGGCCAGACG	CGAATTATTT
6701	TTGATGGCGT	TCCTATTGGT	TAAAAAATGA	GCTGATTTAA	CAAAAATTTA
6751	ACGCGAATTT	TAACAAAATA	TTAACGTTTA	CAATTTAAAT	ATTTGCTTAT
6801	ACAATCTTCC	TGTTTTTGGG	GCTTTTCTGA	TTATCAACOG	GGGTACATAT
6851	GATTGACATG	CTAGTTTTAC	GATTACCGTT	CATCGATTCT	спаттаст
6901	CCAGACTCTC	AGGCAATGAC	CTGATAGCCT	TTGTAGATCT	CTCAAAAATA
6951	GCTACCCTCT	COCCCATGAA	TTTATCAGCT	AGAACGGTTG	AATATCATAT
7001	TGATGGTGAT	TTGACTGTCT	COGGCCTTTC	TCACCCTTTT	GAATCITTAC
7051	CTACACATTA	CTCAGGCATT	GCATTTAAAA	TATATGAGGG	TTCTAAAAAT
7101	TTTTATCCTT	GCGTTGAAAT	AAAGGCTTCT	CCCCCAAAAG	TATTACAGGG
7151	TCATAATGTT	TTTGGTACAA	CCGATTTAGC	TTTATGCTCT	GAGGCTTTAT

Figure 5

COMPLEMENTARY TO M₁₃

DOCITION	5' * 3'	POSITION	
POSITION 645	AGCAACACTATCATA	631	M ₁₃ /1
615	ACGACGATAAAAACC	601	M ₁₃ /2
585	TTTTGCAAAAGAAGT	571	M ₁₃ /3
555 /	AATAGTAAAATGTTT	541	M ₁₃ /4
525	CAATACTGOGGAATG	511	M ₁₃ /5
495	TGAATCCCCTCAAA	481	M ₁₃ /6
465	AGAAAACGAGAATGA	451	M ₁₃ /7
435	CAGGTCTTTACCCTG	421	M ₁₃ /8
405	AGGAAAGOGGATTIGC	391	M ₁₃ /9
375	AGGAAGOOOGAAAGA	361	M ₁₃ /10
		•	
	COMPLEME	NTARY TO SS PHAGE	DNA
POSITION		NTARY TO SS PHAGE POSITION	DNA
POSITION 351	COMPLEMENTS 5' * * 3' ATATTTGAAGTCTTT		DNA M ₁₃ /11
	5' * * 3'	POSITION	
351	5' * * 3' ATATTTGAAGTCTTT * *	POSITION 366	M ₁₃ /11
351 371	5' * * 3' ATATTTGAAGTCTTT TCTTTTTGATGCAAT	POSITION 366 386	M ₁₃ /11 M ₁₃ /12
351 371 391	5' * 3' ATATTTGAAGTCTTT TCTTTTTGATGCAAT CTATAATACTCAGGG	POSITION 366 386 406	M ₁₃ /11 M ₁₃ /12 M ₁₃ /13
351 371 391 411	5' * 3' ATATTTGAAGTCTTT TCTTTTTGATGCAAT CTATAATACTCAGGG TGATTTATGGTCATT	POSITION 366 386 406 426	M ₁₃ /11 M ₁₃ /12 M ₁₃ /13 M ₁₃ /14
351 371 391 411 431	5' * 3' ATATTTGAAGTCTTT TCTTTTTGATGCAAT CTATAATACTCAGGG TGATTTATGGTCATT GTTTAAAGCATTTGA	POSITION 366 386 406 426 446	M ₁₃ /11 M ₁₃ /12 M ₁₃ /13 M ₁₃ /14 M ₁₃ /15
351 371 391 411 431 451	5' 3' ATATTTGAAGTCTTT TCTTTTTGATGCAAT CTATAATACTCAGGG TGATTTATGGTCATT GTTTAAAGCATTTGA TATTTATGACGATTC	POSITION 366 386 406 426 446 466	M ₁₃ /11 M ₁₃ /12 M ₁₃ /13 M ₁₃ /14 M ₁₃ /15 M ₁₃ /16
351 371 391 411 431 451 471	ATATTTGAAGTCTTT TCTTTTTGATGCAAT CTATAATACTCAGGG TGATTTATGGTCATT GTTTAAAGCATTTGA TATTTATGACGATTC TATCCAGTCTAAACA	POSITION 366 386 406 426 446 466 486	M ₁₃ /11 M ₁₃ /12 M ₁₃ /13 M ₁₃ /14 M ₁₃ /15 M ₁₃ /16 M ₁₃ /17

Figure 6

Primers for Nucleic Acid Production Derived from M13mp18 Sequence

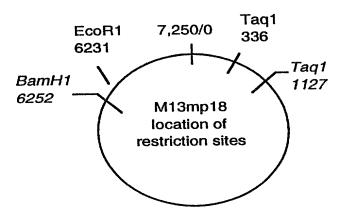
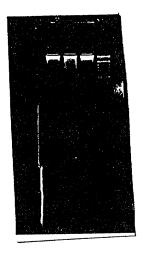


Figure 7

Appropriate M13mp18 Restriction Sites



Lane 1: from calf thymus + Taq digested mp18 amplification reaction

Lane 2: from Taq digested mp18 amplification reaction

Lane 3: from calf thymus amplification reaction

Lane 4: øX174 Hinf1 size marker

Figure 8



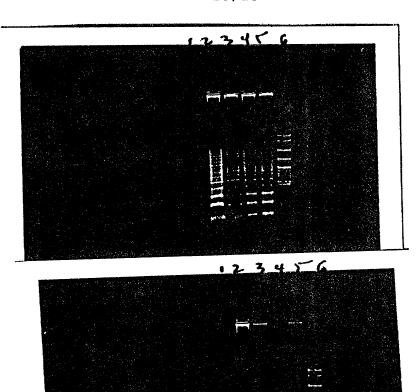
Lane 1: no template

Lane 2: mp18 template, phosphate buffer

Lane 3: Mspl/pBR322 size marker

Lane 4: mp18 template, MOPS buffer

Figure 9



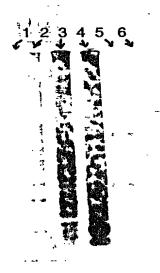
Top= (+) Template
Bottom= (-) Template

Lane 1: phosphate buffer

Lane 2: MES Lane 3: MOPS Lane 4: DMAB Lane 5: DMG

Lane 6: pBR322/Mspl size marker

Figure 10



Lane 1: DMAB buffer, no template

Lane 2: DMAB buffer, mp18 template

Lane 3: DMG buffer, no template

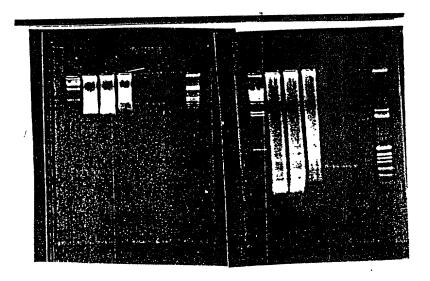
Lane 4: DMG buffer, mp18 template

Lane 5: No reaction

Lane 6: 200 ng Taq I digested mp18

size marker/positive control

Figure 11



First Time Interval Second Time Interval

Agarose Gel Analysis

Lane 1: lambda Hind III marker

Lane 2: Amp/Untreated

Lane 3: Amp/Kinased

Lane 4: Amp/Kinased/Ligated

Lane 5: PCR/Untreated

Lane 6: PCR/Kinased

Lane 7: PCR/Kinased/Ligated Lane 8: øX174/Hinf1 marker

Figure 12

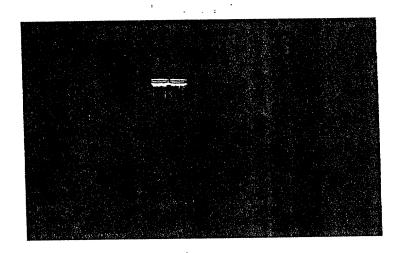
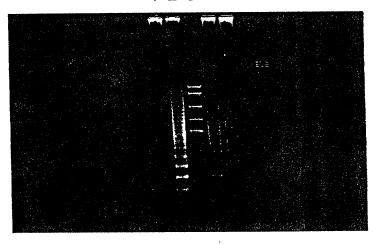


Figure 13

12345 6



Lane 1: Primers alone

Lane 2: Primers + taq digested M13 DNA

Lane 3: Molecular weight markers

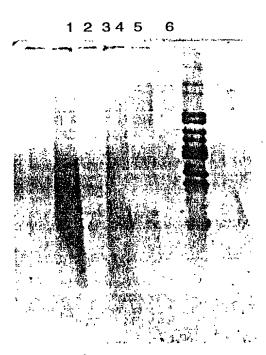
Lane 4: Primers + RNA

Lane 5: Primers alone

Lane 6: M13 digested DNA

Buffer was dimethyl amino glycine, pH 8.6

Figure 14



Lane 1: Primers alone

Lane 2: Primers + taq digested M13 DNA

Lane 3: Molecular weight markers

Lane 4: Primers + RNA

Lane 5: Primers alone

Lane 6: M13 digested DNA

Buffer was dimethyl amino glycine, pH 8.6

Figure 15

Figure 16

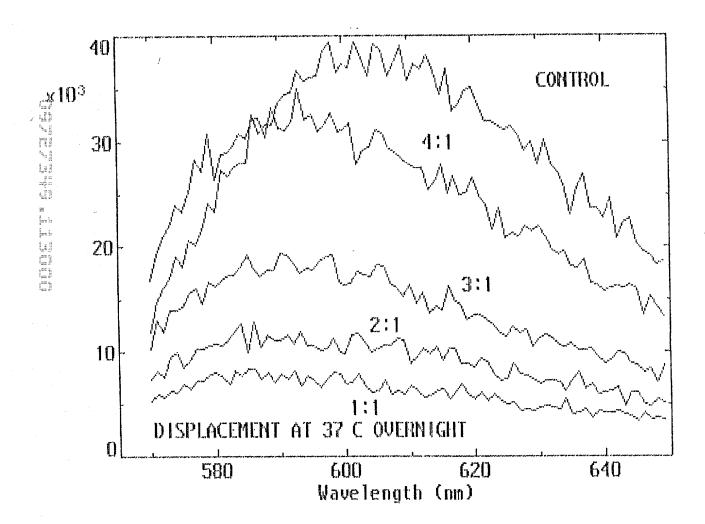


Figure 17

plBl 31-BH5-2

fmet AUG of Lac z {T7 Promotor region.... LAC PROMOTOR..ATG ACC ATG ATT ACG CCA GAT ATC AAA TTA ATA CGA CTC ACT ATA

oligo 50-mer

3'- tac t*aa t*gc ggt* ct*a t*ag t*Vt aat* tat* gct* gag t*ga t*at* c-5' 10 base insert

T7 RNA Start { «« T3 Promotor Region } IGGG CTC ICCT TTA GTG ACG GTT AAT»»} «- T3 Start Signal

pIBI 31 BSII/HCV

{«- T7 Promotor Region }

MULTIPLE CLONING SITE + 390 BASE INSERT CTA /TAG TGA GTC CGT ATT AAT....

«- T7 Start Signal

5'-ct*a t*ag t*ga gt*c gt*a tt*a at*...........